Applied Genome Research

Introduction to Linux

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File sytem organization

- absolute path starts with '/'
- Homes: /homes/<USERNAME>
  - For private data (small files only)
- Course volume: /vol/agrcourse/
  - /vol/agrcourse/bin
    - Contains executable files (tools) used by all participants
  - /vol/agrcourse/scripts
    - Contains scripts (tools) used by all participants
  - /vol/agrcourse/data
    - Contains data used by all participants
  - /vol/agrcourse/members/<USERNAME>
    - Contains data and results produced by specific participant

xterm / lqxterm

- xterm is opened via menu
  - Every command is executed on thinlinc server
  - All users are depending on only two servers
- lqxterm is opened by typing 'lqxterm' into xterm
  - Every command is executed on a powerful computer dedicated to computationally complex tasks
  - Several different computers available
  - Use lqxterm for everything!

xterm / lqxterm

- Default path is homes (/homes/<USERNAME> = ~):
  - zorin:~>
- Commands to be entered into command line are indicated by a leading '$'
- Do not type this '$'! It is just a symbol for the command line
- Units on the command line are separated by space
  - => never use space in names of directory names
- Change into another path:
  - $ cd /absolute_path/sub_dir   change into given directory
  - $ cd sub_dir_name   change into subdirectory
  - $ cd   change into homes
  - $ cd ..   change into parent directory
- Path can be copied from File Manager by marking the text and clicking into the lqxterm with the middle mouse button (wheel)

Running python scripts

- My python scripts are started in the following way:
  - $ python <SCRIPT_NAME>   runs script or opens help if arguments are missing
- Running scripts with arguments:
  - $ python <SCRIPT_NAME> --argument1_name <ARGUMENT1> --argument2_name <ARGUMENT2>
- Script shows help if provided arguments are wrong or insufficient
- EXAMPLE:
  - $ python /vol/agrcourse/scripts/contig_stats.py
- EXERCISE: Analyze the sequence length distribution of the TAIR10.fa (Col-0 reference sequence) file /vol/agrcourse/data/TAIR10.fa !

Permissions

- r = read
- w = write
- x = execute

- Read&write in own directories (/vol/agrcourse/members/xxx/)
- Read(&write) in shared directories (/vol/agrcourse/members/)
- Read only in public directories (e.g. /vol/biotools/)
- Permission to run a script can be checked at 'properties'

Running other tools

- Get help of tool:
  - \$<name_of_tool>
  - \$<name_of_tool> --help
- Providing arguments is different for each tool:
  - Separated by space as shown for python scripts
  - Associated with variable name via '='

- Most tools open help if provided arguments are insufficient or wrong

- EXERCISE: Start SOAPdenovo2 and look at the help!

Running java tools

- Starting tool to get help:
  - $ java -Xmx8g –jar <NAME>.jar –help
- EXERCISE: Start trimmomatic to get the help information displayed!

Filezilla

All actions

Local file system

Remote file system

Drag&Drop

History of file transfer